Please substitute the paragraph under the subtitle "CROSS REFERENCE TO RELATED APPLICATIONS" on page 1 with the following amended version:

C1

--This application is a 371 of PCT/US99/04549, filed March 2, 1999, and claims priority from USSN 60/076,621, filed March 3, 1998, now abandoned, herein incorporated by reference in its entirety.--

Please substitute the paragraph starting on page 19 line 14 and ending on page 20 line 2 with the following amended version:

C2

-- Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a word length (W) of 11, the BLOSUM62 scoring matrix (*see* Henikoff

C2

& Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.--

IN THE CLAIMS:

Please cancel claims 5 and 8-35 without prejudice to subsequent revival.

Please substitute claims 1 and 6 with the following amended version:

C3

1. (Once amended) An isolated nucleic acid encoding a polypeptide monomer comprising an alpha subunit of a potassium channel, the polypeptide monomer:

(i) forming, with at least one additional Kir alpha subunit, a potassium channel having the characteristic of inward rectification; and

(ii) encoded by a nucleic acid that selectively hybridizes under highly stringent hybridization conditions to a nucleotide sequence of SEQ ID NO:2, wherein the stringent conditions comprise incubation at 42°C in a solution comprising 50% formamide, 5 x SSC, and 1% SDS or an incubation at 65°C in a solution comprising 5 x SSC and 1% SDS at 65°C with a wash in 0.2 x SSC and 0.1% SDS.

C4

6. (Once Amended) The isolated nucleic acid of claim 1, wherein the nucleic acid encodes a polypeptide monomer having a molecular weight of about between 38 kDa to 48 kDa, wherein the molecular weight is predicted based on amino acid sequence.

IN THE ABSTRACT:

Following the sequence listing ending on page 65, please add the following:

-- NUCLEIC ACID ENCODING HUMAN KIR5.1

ABSTRACT OF THE DISCLOSURE